IFWO

RAW SEQUENCE LISTING DATE: 08/23/2004
PATENT APPLICATION: **US/10/770,639** TIME: 16:41:31

Input Set : **A:\27331-501CIP2A.ST25.txt**
Output Set: **N:\CRF4\08232004\J770639.raw**

<110> APPLICANT: Sanchez-Madrid, Francisco
Martinez Alonso, Carlos
Sancho Madrid, David
Engel Rocamora, Pablo
Esplugues Artola, Enric
Vega Ramos, Javier
Lauzurica Gomez, Pilar
<120> TITLE OF INVENTION: Immune Regulation Based on the Targeting of Early Activation Molecules
<130> FILE REFERENCE: 27331-501CIP2A
<140> CURRENT APPLICATION NUMBER: 10/770639
<141> CURRENT FILING DATE: 2004-02-02
<150> PRIOR APPLICATION NUMBER: ES 200300252
<151> PRIOR FILING DATE: 2003-01-31
<150> PRIOR APPLICATION NUMBER: ES 200302587
<151> PRIOR FILING DATE: 2003-11-05
<160> NUMBER OF SEQ ID NOS: 6
<170> SOFTWARE: PatentIn version 3.2

ENTERED

<210> SEQ ID NO: 1
<211> LENGTH: 1702
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 1

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ttgcatccgg agagtggaca agaaaatgat gccaccagtc cccatttctc aacacgtcat 180
gaagggtcct tccaagttcc tgtcctgtgt gctgtaatga atgtggtctt catcaccatt 240
ttaatcatag ctctcattgc cttatcagtg ggccaataca attgtccagg ccaatacaca 300
ttctcaatgc catcagacag ccatgtttct tcatgctctg aggactgggt tggctaccag 360
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tctgaacatg gtgctactct tgctgtcatt gattctgaaa aggacatgaa ctttctaaaa 480
cgatacgcag gtagagagga acactgggtt ggactgaaaa aggaacctgg tcacccatgg 540
aagtggtcaa atggcaaaga atttaacaac tggttcaacg ttacagggtc tgacaagtgt 600
gtttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaattt atactggata 660
tgtaacaaac cttacaaata ataaggaaac atgttcactt attgactatt atagaatgga 720
actcaaggaa atctgtgtca gtggatgctg ctctgtggtc cgaagtcttc catagagact 780
ttgtgaaaaa aaattttata gtgtcttggg aattttcttc caaacagaac tatggaaaaa 840
aaggaagaaa ttccaggaaa atctgcactg tgggctttta ttgccatgag ctagaagcat 900
cacaggttga ccaataacca tgcccaagaa tgagaagaat gactatgcaa cctttggatg 960
cactttatat tattttgaat ccagaaataa tgaaataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcatgcatt tgcactactg gaaggagtta 1080
gatgttggta ctagatactg aatgtaaaca aaggaattat ggctggtaac ataggttttt 1140
agtctaattg aatcccttaa actcagggag catttataaa tggacaaatg cttatgaaac 1200

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 75 taagatttgt aatatttctc tcttttaga gaaatttgcc aatttacttt gttatttttc   1260
 77 cccaaaaaga atgggatgat cgtgtattta ttttttact tcctcagctg tagacaggtc   1320
 79 cttttcgatg gtacatattt ctttgccttt ataatctttt atacagtgtc ttacagagaa   1380
 81 aagacataag caaagactat gaggaatatt tgcaagacat agaatagtgt tggaaaatgt   1440
 83 gcaatatgtg atgtggcaaa tctctattag gaaatattct gtaatcttca gacctagaat   1500
 85 aatactagtc ttataatagg tttgtgactt tcctaaatca attctattac gtgcaatact   1560
 87 tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt   1620
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 91 aaaaaaaaaa aaaaaaaaaa aa                                          1702
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 95 <211> LENGTH: 199
 96 <212> TYPE: PRT
 97 <213> ORGANISM: Homo sapiens
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105 Glu Ser Gly Gln Glu Asn Asp Ala Thr Ser Pro His Phe Ser Thr Arg
106             20                  25                  30
109 His Glu Gly Ser Phe Gln Val Pro Val Leu Cys Ala Val Met Asn Val
110         35                  40                  45
113 Val Phe Ile Thr Ile Leu Ile Ile Ala Leu Ile Ala Leu Ser Val Gly
114     50                  55                  60
117 Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Ser Asp Ser
118 65                  70                  75                  80
121 His Val Ser Ser Cys Ser Glu Asp Trp Val Gly Tyr Gln Arg Lys Cys
122                 85                  90                  95
125 Tyr Phe Ile Ser Thr Val Lys Arg Ser Trp Thr Ser Ala Gln Asn Ala
126             100                 105                 110
129 Cys Ser Glu His Gly Ala Thr Leu Ala Val Ile Asp Ser Glu Lys Asp
130         115                 120                 125
133 Met Asn Phe Leu Lys Arg Tyr Ala Gly Arg Glu Glu His Trp Val Gly
134     130                 135                 140
137 Leu Lys Lys Glu Pro Gly His Pro Trp Lys Trp Ser Asn Gly Lys Glu
138 145                 150                 155                 160
141 Phe Asn Asn Trp Phe Asn Val Thr Gly Ser Asp Lys Cys Val Phe Leu
142                 165                 170                 175
145 Lys Asn Thr Glu Val Ser Ser Met Glu Cys Glu Lys Asn Leu Tyr Trp
146             180                 185                 190
149 Ile Cys Asn Lys Pro Tyr Lys
150         195
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154 <211> LENGTH: 759
155 <212> TYPE: DNA
156 <213> ORGANISM: Homo sapiens
158 <400> SEQUENCE: 3
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161 aagagagttt ctgcaagaca tgacacaaag ctgctagcag aaaatcaaaa cgctgattaa    120
163 aagaagcacg gtatgatgac caaacataaa aagtgtttta taattgttgg tgttttaata    180
165 acaactaata ttattactct gatagttaaa ctaactcgag attctcagag tttatgcccc    240
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167 tatgattgga ttggtttcca aaacaaatgc tattatttct ctaaagaaga aggagattgg    300
169 aattcaagta aatacaactg ttccactcaa catgccgacc taactataat tgacaacata    360
171 gaagaaatga attttcttag gcggtataaa tgcagttctg atcactggat tggactgaag    420
173 atggcaaaaa atcgaacagg acaatgggta catggagcta catttaccaa atcgtttggc    480
175 atgagaggga gtgaaggatg tgcctacctc agcgatgatg gtgcagcaac agctagatgt    540
177 tacaccgaaa gaaaatggat ttgcaggaaa agaatacact aagttaatgt ctaagataat    600
179 ggggaaaata gaaaataaca ttattaagtg taaaaccagc aaagtacttt tttaattaaa    660
181 caaagttcga gttttgtacc tgtctggtta attctgctta cgtgtcaggc tacacataaa    720
183 agccacttca aagattggca aaaaaaaaaa aaaaaaaaa                          759
186 <210> SEQ ID NO: 4
187 <211> LENGTH: 149
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <400> SEQUENCE: 4
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194 1               5                  10                  15
197 Thr Thr Asn Ile Ile Thr Leu Ile Val Lys Leu Thr Arg Asp Ser Gln
198             20                  25                  30
201 Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr
202         35                  40                  45
205 Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser
206     50                  55                  60
209 Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn
210 65                  70                  75                  80
213 Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys
214                 85                  90                  95
217 Met Ala Lys Asn Arg Thr Gly Gln Trp Val His Gly Ala Thr Phe Thr
218             100                 105                 110
221 Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp
222         115                 120                 125
225 Asp Gly Ala Ala Thr Ala Arg Cys Tyr Thr Glu Arg Lys Trp Ile Cys
226     130                 135                 140
229 Arg Lys Arg Ile His
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234 <211> LENGTH: 850
235 <212> TYPE: DNA
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 5
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241 gcctgcaaac ccaggttgtc tgcattcaaa agagcattct attaaagcta ccttaatttg    120
243 gcgcttattt ttcttaatca tgtttctgac aatcatagtg tgtggaatgg ttgctgcttt    180
245 aagcgcaata agagctaact gccatcaaga gccatcagta tgtcttcaag ctgcatgccc    240
247 agaaagctgg attggttttc aaagaaagtg tttctatttt tctgatgaca ccaagaactg    300
249 gacatcaagt cagaggtttt gtgactcaca agatgctgat cttgctcagg ttgaaagctt    360
251 ccaggaactg aatttcctgt tgagatataa aggcccatct gatcactgga ttgggctgag    420
253 cagagaacaa ggccaaccat ggaaatggat aaatggtact gaatggacaa gacagtttcc    480
255 tatcctggga gcaggagagt gtgcctattt gaatgacaaa ggtgccagta gtgccaggca    540
257 ctacacagag aggaagtgga tttgttccaa atcagatata catgtctaga tgttacagca    600
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259 aagccccaac taatctttag aagcatattg gaactgataa ctccatttta aaatgagcaa 660
261 agaatttatt tcttatacca acaggtatat gaaaatatgc tcaatatcac taataactgg 720
263 gaaaatacaa atcaaaatca tagtaaaata ttacctgttt tcatggtgct aatattacct 780
265 gttctcccac tgctaatgac atacccgaga atgagtaatt tataaataaa agagatttaa 840
267 ttgaaaaaaa 850
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271 <211> LENGTH: 191
272 <212> TYPE: PRT
273 <213> ORGANISM: Homo sapiens
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277 Met His Asp Ser Asn Asn Val Glu Lys Asp Ile Thr Pro Ser Glu Leu
278 1               5                  10                  15
281 Pro Ala Asn Pro Gly Cys Leu His Ser Lys Glu His Ser Ile Lys Ala
282             20                  25                  30
285 Thr Leu Ile Trp Arg Leu Phe Phe Leu Ile Met Phe Leu Thr Ile Ile
286         35                  40                  45
289 Val Cys Gly Met Val Ala Ala Leu Ser Ala Ile Arg Ala Asn Cys His
290     50                  55                  60
293 Gln Glu Pro Ser Val Cys Leu Gln Ala Ala Cys Pro Glu Ser Trp Ile
294 65                  70                  75                  80
297 Gly Phe Gln Arg Lys Cys Phe Tyr Phe Ser Asp Asp Thr Lys Asn Trp
298                 85                  90                  95
301 Thr Ser Ser Gln Arg Phe Cys Asp Ser Gln Asp Ala Asp Leu Ala Gln
302             100                 105                 110
305 Val Glu Ser Phe Gln Glu Leu Asn Phe Leu Leu Arg Tyr Lys Gly Pro
306         115                 120                 125
309 Ser Asp His Trp Ile Gly Leu Ser Arg Glu Gln Gly Gln Pro Trp Lys
310     130                 135                 140
313 Trp Ile Asn Gly Thr Glu Trp Thr Arg Gln Phe Pro Ile Leu Gly Ala
314 145                 150                 155                 160
317 Gly Glu Cys Ala Tyr Leu Asn Asp Lys Gly Ala Ser Ser Ala Arg His
318                 165                 170                 175
321 Tyr Thr Glu Arg Lys Trp Ile Cys Ser Lys Ser Asp Ile His Val
322             180                 185                 190
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